IN THE CLAIMS:

Claims 1, 3-10, 12-15 and 16-22 are presently pending.

Listing of the Claims:

- 1. (currently amended) A genetically transformed plant, comprising:
- a means for modulating mitochondrially generated acetyl-CoA and/or respiration rate in the genetically transformed plant as compared to a genomically-unmodified plant of the same genotype wherein the means for modulating mitochondrially generated acetyl-CoA and/or respiration rate is a nucleic acid sequence incorporated into the plant's genome having a sequence selected from the group of sequences consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4; and
- a promoter operatively linked to the means for reducing plant respiration modulating mitochondrially generated acetyl-CoA and/or respiration rate.
- 2. (canceled) The genetically transformed plant of claim 1, wherein the means for modulating mitochondrially generated acetyl-CoA and/or respiration rate is a nucleic acid incorporated into the plant's genome having a sequence selected from the group of sequences consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4.
- 3. (currently amended) The genetically transformed plant of claim 1, wherein the plant is selected from the group consisting of borage, Canola, castor, cocoa bean, corn, cotton, *Crambe* spp., *Cuphea* spp., flax, *Lesquerella* and *Limnanthes* spp., Linola, nasturtium, *Oenothera* spp., olive, palm, peanut, rapeseed, safflower, soybean, sunflower, tobacco, *Vernonia* spp., wheat, barley, rice, oat, sorghum, rye, and other members of the *Gramineae*.
 - 4. (original) The genetically transformed plant of claim 3, wherein the plant is Canola.
- 5. (currently amended) The genetically transformed plant of claim 1, wherein the means for modulating mitochondrially generated acetyl-CoA and/or respiration rate <u>further</u> includes a gene encoding a pyruvate dehydrogenase kinase oriented in an anti-sense direction.

- 6. (original) The genetically transformed plant of claim 1, wherein the promoter is a ubiquitin gene promoter.
- 7. (original) The genetically transformed plant of claim 1, wherein the promoter is a phaseolin promoter.
- 8. (currently amended) A process for modulating mitochondrially generated acetyl-CoA and/or respiration rate in a transgenic plant, the process comprising: cloning a gene encoding a *Brassica* pyruvate dehydrogenase kinase protein into a vector, wherein the gene comprises a sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4; positioning the gene in an anti-sense orientation within the vector; and

positioning the gene in an anti-sense orientation within the vector; and transforming a plant with the vector to produce the transgenic plant.

- 9. (original) The process according to claim 8, further comprising: linking a promoter to the gene.
- 10. (original) The process according to claim 9, wherein the promoter is a ubiquitin gene promoter or a phaseolin promoter.
- 11. (canceled) The process according to claim 8, wherein the gene has a sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4.
- 12. (original) The process according to claim 8, wherein the plant is selected from the group consisting of borage, Canola, castor, cocoa bean, corn, cotton, *Crambe* spp., *Cuphea* spp., flax, *Lesquerella* and *Limnanthes* spp., Linola, nasturtium, *Oenothera* spp., olive, palm, peanut, rapeseed, safflower, soybean, sunflower, tobacco, *Vernonia* spp., wheat, barley, rice, oat, sorghum, rye, and other members of the *Gramineae*.

- 13. (original) The process according to claim 12, wherein the plant is Canola.
- 14. (original) A transgenic plant obtained by the process according to claim 8.
- 15. (currently amended) A process for modulating mitochondrially generated acetyl-CoA and/or respiration rate in a transgenic plant, the process comprising: cloning a gene encoding a *Brassica* pyruvate dehydrogenase kinase protein into a vector, wherein the gene comprises a sequence selected from the group of sequences consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4;

transforming the vector into a plant to produce the transgenic plant; and

reducing production of the *Brassica* pyruvate dehydrogenase kinase protein in the transgenic plant; and

transforming the vector into a plant to produce the transgenic plant.

- 16. (canceled) The process according to claim 15, wherein the gene has a sequence selected from the group of sequences consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4.
- 17. (original) The process according to claim 15, wherein the plant is selected from the group consisting of borage, Canola, castor, cocoa bean, corn, cotton, *Crambe* spp., *Cuphea* spp., flax, *Lesquerella* and *Limnanthes* spp., Linola, nasturtium, *Oenothera* spp., olive, palm, peanut, rapeseed, safflower, soybean, sunflower, tobacco, *Vernonia* spp., wheat, barley, rice, oat, sorghum, rye, and other members of the *Gramineae*.
 - 18. (original) The process according to claim 17, wherein the plant is Canola.
- 19. (original) The process according to claim 15, wherein the step for reducing production of the *Brassica* pyruvate dehydrogenase kinase protein comprises positioning the gene encoding the *Brassica* pyruvate dehydrogenase kinase protein in an anti-sense orientation in

the vector.

- 20. (currently amended) A transgenic plant produced by the process according to claim 15.
- 21. (previously presented) A combination of DNA fragments comprising SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4.
- 22. (New) A genetically transformed plant, comprising:

a means for modulating mitochondrially generated acetyl-CoA and/or respiration rate in the genetically transformed plant as compared to a genomically-unmodified plant of the same genotype wherein the means for modulating mitochondrially generated acetyl-CoA and/or respiration rate is a nucleic acid incorporated into the plant's genome having a sequence of SEQ ID NO:1; and

a promoter operatively linked to the means for modulating mitochondrially generated acetyl-CoA and/or respiration rate.